



SEQUENCE LISTING #4

<110> Tang et al.

<120> METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

<130> 28110/37260A

<140>

<141> 2001-06-28

<150> To be assigned

<151> 2001-04-05

<150> 60/266,614

<151> 2001-02-05

<150> 60/215,733

<151> 2000-06-28

<150> 09/757,562

<151> 2001-01-09

<150> 09/543,774

<151> 2000-04-05

<160> 48

<170> PatentIn version 3.0

a
<210> 1
<211> 301
<212> DNA
<213> Homo sapiens

<400> 1
gcacgagacg aggaaaaaaaaa ggaagggaga ggaaaaagaaa aaaacctaatt aaaggagaaaa 60
gtaaagaagc aataacctgac agcaaaaagtc tggatccag caaagaaatc ccagagcaac 120
gagaaaaacaa acagcagcag aagaagcgaa aagtccaaga taaacagaaaa tcggtatcag 180
tcagcactgt acactagagg gttccatgag attattgttag actcatgatg ctgctatctc 240
aaccagatgc ccaggacagg tgctctagcc attaggacca caaatggaca tgtcagttat 300
t 301

<210> 2
<211> 392
<212> DNA
<213> Homo sapiens

<400> 2
tggaaactcgata tatccagata taaaataagcg tacaaaatgc aaagctgact gtgatacctg 60
tttcaacaaa gatttctgca caaaaatgtaa aagtggattt tacttacacc ttggaaagtg 120
cctgacaat tgcccagaag ggttggaaagc caacaaccat actatggagt gtgtcagttat 180
tgtgcactgt gaggtcagtg aatggaatcc ttggagtcca tgcacgaaga agggaaaaac 240
atgtggcttc aaaagagggta 3 ctgaaacacg ggtccgagaa ataatacagc atccttcagc 300
aaaggtaac ctatgtcccc caacaaatga gacaagaaag tgtacagtgc aaaggaagaa 360
gtgtcagaag ggagaacgag gaaaataagg ag 392

<210> 3
<211> 475
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)..(475)
<223> n = A, T, G, or C

<400> 3
gtnagtaccc ccagggattt cactgagngc ctggactgag gaccgcgtcna anngcnngan 60
ccacgcgtnc gcccacgcgt ccggagagga aaagaaaaaa acctaattta ggagaaagta 120
aagaagcaat acctgacagc ggaagtctgg aatggagcaa agaaatccca gagcaacgag 180
aaaacaaaca gcagcagaag aagcgaaaag tccaaagataa acagaaatcg gtatcagtca 240
gcactgtaca ctagagggtt ccatgagatt atttagact catgatgtc ctatctcaac 300
cagatgccca ggacaggtgc tctagccatt aggaccacaa atggacatgt cagttattgc 360
tctgtctaaa caacattccc agtagttgct atattttca tacaagcata gttaacaaca 420
aagagccaaa agatcaaaga agggatactt tcagatggtt gtcttgttg cttcn 475

<210> 4
<211> 473
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)..(473)
<223> n = A, T, G, or C

<400> 4
tggcannnn aaantttga nattcgatcc gcgctgcagg aattcggcac gagacgagga 60

aaaaaaggaa gggagaggaa aagaaaaaaaa cctaataaag gagaaagtaa agaagcaata 120
cctgacagca aaagtctgga atccagcaga gaaatccag agcaacgaga aaacaaacag 180
cagcagaaga agcgaaaagt ccaagataaa cagaaatcg tagactcgact cactgtacac 240
tagagggttc catgagatta ttgttagactc atgatgctgc tatctcaacc agatgcccag 300
gacaggtgct ctagccatta ggaccacaaa tggacatgtc agttattgct ctgtctaaac 360
aacattccca gtagttgcta tattcttcat acaagcatag ttaacaacaa agagccaaaa 420
gatcaaagaa gggatactt cagatggttg tcttgtgtc ttctctgcat ttt 473

<210> 5
<211> 462
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(462)
<223> n = A, T, G, or C

<400> 5
tgggagannn ntttggaaact gagatcgctg canacncnac nangaataaa aggaagggag 60
agggaaagaa aaaaacctaa taaaggagaa agtaaagaat caatttctga cagcaaaagt 120
ctggaatcca tcaaagaaat cccatatcaa cgagaaaaca gacagcagca caaaaagcga 180
aaagtccaag ataaacagaa atcggtatca gtcagcactg tacactagag gttccatga 240
gattattgtt gactcatgtat gctgttatct caaccagatg cccaggacag gtgtctatc 300
cattacgacc acaaatggac atgtcagttt ttgctctgtc taaacaacat tcccagtagt 360
tgctatattt ttcatacaag catagttaac aacaaagagc caaaagatca aagaagggat 420
actttcagat gttgtctt gttgtctc tgcattttta aa 462

<210> 6
<211> 384
<212> DNA
<213> Homo sapiens

<400> 6
aataatgtgt aaaaaatgca aagctgactg tgataacctgt ttcaacaaaa atttctgcac 60
aaaatgtaaa agtggatttt acttacacct tggaaagtgc cttgacaatt gcccagaagg 120
gttggaaagcc aacaaccata ctatggagtg tgcacttatt gtgcactgtg aggtcagtga 180
atggaatcct tggagtcacat gcacgaagaa gggaaaaaca tgcgtttca aaagagggac 240

tgaaacacgg gtccgagaaa taatacagca tccttcagca aagggttaacc tatgtcccc	300
aacaaatgag acaagaaaagt gtacagtgc aaggaagaag tgtcagaagg gagaacgagg	360
aaaaaaagga agggagagga aaag	384
<210> 7	
<211> 390	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> misc_feature	
<222> (1)..(390)	
<223> n = A, T, G, or C	
<400> 7	
cgttgctctg ggatttcttt gctggattcc agactttgc tgtcaggtat tgcttctta	60
ctttctcctt tattaggttt ttttctttc ctctcccttc cttttttcc tcgttctccc	120
ttctgacact tttcccttg cactgtacac tttcttgtct catttgttgg gggacatagg	180
ttaccctttg ctgaaggatg ctgttattatt tctcggaccc gtgtttcagt ccctctttg	240
aagccacatg ttttccctt cttcgtgcat ggactccaag gattccattc actgacctca	300
cagtgaccaa tactgacaca ctccatagta tggttgttgg cttccaaccc ttctggcaa	360
ttgtcaaggc actttccaag gtgttaagtan	390
<210> 8	
<211> 1345	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> misc_feature	
<222> (321)..(1235)	
<223> similar to gi4519541 in the genpept database release 114, Run with FASTXY3.3t00, default parameter	
<400> 8	
gcggccgccc cggcggtcc tggAACCCCG gttcgccgcg atgccagcca ccccaagcgaa	60
gccggccgcag ttcatgtcgtt ggataatttg aaagtacaat agttggtttc cctgtccacc	120
cgcggccactt cgcttgccat cacagcacgc ctatcgatg tgagaggaga agtcccgcgt	180
ctcgccact gtctatatac gcctaaccacc tacatatatt taaaaacat taaatataat	240
taacaatcaa aagaaagagg agaaaggaag ggaagcatta ctgggttact atgcacttgc	300
gactgatttc ttggctttt atcattttga actttatgga atacatcgac agccaaaacg	360

cctccccggg aaggcgccag cgaagaatgc atcctaacgt tagtcaaggc tgccaaggag 420
gctgtgcaac atgctcagat tacaatggat gtttgcata taagcccaga ctatttttg 480
ctctggaaag aattggcatg aagcagattg gagtatgtct catcttcata tccaaatgtgga 540
tattatggaa ctcgatatacc agatataaat aatgtgtaca aaatgcaaag ctgactgtga 600
tacctgtttc aacaaaaatt tctgcacaaa atgtaaaagt ggatttact tacaccttgg 660
aaagtgcctt gacaattgcc cagaagggtt ggaagccaaac aaccatacta tggagtgtgt 720
cagttatgtg cactgtgagg tcagtgaatg gaatccttgg agtccatgca cgaagaagg 780
aaaaacatgt ggcttcaaaa gagggactga aacacgggtc cgagaaataa tacagcatcc 840
ttcagcaaag ggttaacctat gtcccccaac aaatgagaca agaaagtgtc cagtgc当地 900
gaagaagtgt cagaagggag aacgagggaaa aaaagggagg gagagggaaa gaaaaaaaacc 960
taataaagga gaaagtaaag aagcaatacc tgacagcaaa agtctggat ccagcaaaga 1020
aatcccagag caacgagaaa acaaacagca gcagaagaag cgaaaagtcc aagataaaca 1080
gaaatcggtc tcagtcagca ctgtacacta gagggttcca tgagattatt gtagactcat 1140
gatgctgcta tctcaaccag atgcccagga caggtgctct agccattagg accacaaatg 1200
gacatgtcag ttattgctct gtctaaacaa cattcccagt agttgctata ttcttcatac 1260
aagcatagtt aacaacaaag agccaaaaga tcaaagaagg gatactttca gatgggtgtc 1320
ttgtgtgctt ctctgcattt ttaaa 1345

<210> 9
<211> 1343
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS

<222> (291) . . (1109)

<400> 9

```

gccggccgac ttcagtgcctt ggataatttg aaagtacaat agttggtttc cctgtccacc 120
cgccccactt cgcttgccat cacagcacgc ctatcgatg tgagaggaga agtcccgtg 180
ctcgggcact gtctatatac gcctaaccacc tacatataattt taaaaaacat taaatataat 240
taacaatcaa aagaaagagg agaaaggaag ggaagcatta ctgggttact atg cac
                                         Met His
                                         1

```

```

ttg cga ctg att tct tgg ctt ttt atc att ttg aac ttt atg gaa tac 344
Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met Glu Tyr
      5          10          15

```

atc ggc agc caa aac gcc tcc cgg gga agg cgc cag cga aga atg cat Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg Met His 20 25 30	392
cct aac gtt agt caa ggc tgc caa gga ggc tgt gca aca tgc tca gat Pro Asn Val Ser Gln Gly Cys Gln Gly Cys Ala Thr Cys Ser Asp 35 40 45 50	440
tac aat gga tgt ttg tca tgt aag ccc aga cta ttt ttt gct ctg gaa Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala Leu Glu 55 60 65	488
aga att ggc atg aag cag att gga gta tgt ctc tct tca tgt cca agt Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys Pro Ser 70 75 80	536
gga tat tat gga act cga tat cca gat ata aat aag tgt aca aaa tgc Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr Lys Cys 85 90 95	584
aaa gct gac tgt gat acc tgt ttc aac aaa aat ttc tgc aca aaa tgt Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys 100 105 110	632
aaa agt gga ttt tac tta cac ctt gga aag tgc ctt gac aat tgc cca Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn Cys Pro 115 120 125 130	680
gaa ggg ttg gaa gcc aac aac cat act atg gag tgt gtc agt att gtg Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser Ile Val 135 140 145	728
cac tgt gag gtc agt gaa tgg aat cct tgg agt cca tgc acg aag aag His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr Lys Lys 150 155 160	776
gga aaa aca tgt ggc ttc aaa aga ggg act gaa aca cgg gtc cga gaa Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val Arg Glu 165 170 175	824
ata ata cag cat cct tca gca aag ggt aac cta tgt ccc cca aca aat Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro Thr Asn 180 185 190	872
gag aca aga aag tgt aca gtg caa agg aag aag tgt cag aag gga gaa Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys Gly Glu 195 200 205 210	920
cga gga aaa aaa gga agg gag agg aaa aga aaa aaa cct aat aaa gga Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Pro Asn Lys Gly 215 220 225	968
gaa agt aaa gaa gca ata cct gac agc aaa agt ctg gaa tcc agc aaa Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser Ser Lys 230 235 240	1016
gaa atc cca gag caa cga gaa aac aaa cag cag cag aag aag cga aaa Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Lys Lys Arg Lys 245 250 255	1064

gtc caa gat aaa cag aaa tcg gta tca gtc agc act gta cac tag	1109
Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val His	
260	265
270	
agggttccat gagattattg tagactcatg atgctgctat ctcaccaga tgcccaggac	1169
aggtgctcta gccattagga ccacaaatgg acatgtcagt tattgctctg tctaaacaac	1229
attcccagta gttgctatat tcttcataca agcatagtt acaacaaaga gccaaaagat	1289
caaagaaggg atactttcag atggttgtct tgtgtgcttc tctgcatttt taaa	1343

<210> 10
 <211> 272
 <212> PRT
 <213> Homo sapiens

<400> 10

Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met	
1	5
10	15

Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg	
20	25
30	

Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys	
35	40
45	

Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala	
50	55
60	

Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys	
65	70
75	80

Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr	
85	90
95	

Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr	
100	105
110	

Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn	
115	120
125	

Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser	
130	135
140	

Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr	
145	150
155	160

Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val
165 170 175

Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro
180 185 190

Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys
195 200 205

Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn
210 215 220

Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser
225 230 235 240

Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys
245 250 255

Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val His
260 265 270

<210> 11
<211> 819

<212> DNA

<213> Homo sapiens

<400> 11
atgcacttgc gactgatttc ttggcttttt atcatttga actttatgga atacatcgcc 60
agccaaaacg cctcccgggg aaggcgccag cgaagaatgc atcctaacgt tagtcaaggc 120
tgccaaggag gctgtgcaac atgctcagat tacaatggat gtttgcataa taagccaga 180
ctattttttg ctctggaaag aattggcatg aagcagattg gagttatgtct ctcttcatgt 240
ccaagtggat attatggAAC tcgatatcca gatataaata agtgtacaaa atgcaaagct 300
gactgtgata cctgtttcaa caaaaatttc tgcacaaaat gtaaaagtgg attttactta 360
caccttggaa agtgccttga caattgccccaa gaagggttgg aagccaaacaa ccatactatg 420
gagtgtgtca gtattgtgca ctgtgaggc agtgaatgga atccttggag tccatgcacg 480
aagaaggaa aaacatgtgg cttcaaaaga gggactgaaa cacgggtccg agaaataata 540
cagcatcctt cagcaaaggtaaacatgt ccccaacaa atgagacaag aaagtgtaca 600
gtgcaaagga agaagtgtca gaagggagaa cgaggaaaaa aaggaaggaa gaggaaaaga 660
aaaaaaccta ataaaggaga aagtaaagaa gcaatacctg acagcaaaag tctggaatcc 720

agcaaagaaa tcccagagca acgagaaaac aaacagcagc agaagaagcg aaaagtccaa	780
gataaacaga aatcggtatc agtcagcact gtacactag	819
<210> 12	
<211> 822	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> (1)...(822)	
<400> 12	
atg ggt cac ttg cga ctg att tct tgg ctt ttt atc att ttg aac ttt	48
Met Gly His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe	
1 5 10 15	
atg gaa tac atc ggc agc caa aac gcc tcc cgg gga agg cgc cag cga	96
Met Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg	
20 25 30	
aga atg cat cct aac gtt agt caa ggc tgc caa gga ggc tgt gca aca	144
Arg Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr	
35 40 45	
tgc tca gat tac aat gga tgt ttg tca tgt aag ccc aga cta ttt ttt	192
Cys Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe	
50 55 60	
gct ctg gaa aga att ggc atg aag cag att gga gta tgt ctc tct tca	240
Ala Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser	
65 70 75 80	
tgt cca agt gga tat tat gga act cga tat cca gat ata aat aag tgt	288
Cys Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys	
85 90 95	
aca aaa tgc aaa gct gac tgt gat acc tgt ttc aac aaa aat ttc tgc	336
Thr Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys	
100 105 110	
aca aaa tgt aaa agt gga ttt tac tta cac ctt gga aag tgc ctt gac	384
Thr Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp	
115 120 125	
aat tgc cca gaa ggg ttg gaa gcc aac aac cat act atg gag tgt gtc	432
Asn Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val	
130 135 140	
agt att gtg cac tgt gag gtc agt gaa tgg aat cct tgg agt cca tgc	480
Ser Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys	
145 150 155 160	
acg aag aag gga aaa aca tgt ggc ttc aaa aga ggg act gaa aca cgg	528
Thr Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg	
165 170 175	

gtc cga gaa ata ata cag cat cct tca gca aag ggt aac cta tgt ccc 576
Val Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro
180 185 190

cca aca aat gag aca aga aag tgt aca gtg caa agg aag aag tgt cag 624
Pro Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln
195 200 205

aag gga gaa cga gga aaa aaa gga agg gag agg aaa aga aaa aaa cct 672
Lys Gly Glu Arg Gly Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro
210 215 220

aat aaa gga gaa agt aaa gaa gca ata cct gac agc aaa agt ctg gaa 720
Asn Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu
225 230 235 240

tcc agc aaa gaa atc cca gag caa cga gaa aac aaa cag cag cag aag 768
Ser Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Lys
245 250 255

aag cga aaa gtc caa gat aaa cag aaa tcg gta tca gtc agc act gta 816
Lys Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val
260 265 270

cac tag 822
His

<210> 13
<211> 273

<212> PRT
<213> Homo sapiens

<400> 13

Met Gly His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe
1 5 10 15

Met Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg
20 25 30

Arg Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr
35 40 45

Cys Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe
50 55 60

Ala Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser
65 70 75 80

Cys Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys
85 90 95

Thr Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys
100 105 110

Thr Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp
115 120 125

Asn Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val
130 135 140

Ser Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys
145 150 155 160

Thr Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg
165 170 175

Val Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro
180 185 190

Pro Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln
195 200 205

Lys Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro
210 215 220

Asn Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu
225 230 235 240

Ser Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Lys
245 250 255

Lys Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val
260 265 270

His

<210> 14
<211> 160

<212> PRT
<213> Homo sapiens

<400> 14

Cys Thr Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe
1 5 10 15

Cys Thr Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu
20 25 30

Asp Asn Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys
35 40 45

Val Ser Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro
50 55 60

Cys Thr Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr
65 70 75 80

Arg Val Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys
85 90 95

Pro Pro Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys
100 105 110

Gln Lys Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys
115 120 125

Pro Asn Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu
130 135 140

Glu Ser Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln
145 150 155 160

<210> 15

<211> 21

<212> PRT

<213> Homo sapiens

<400> 15

Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met
1 5 10 15

Glu Tyr Ile Gly Ser

20

<210> 16

<211> 251

<212> PRT

<213> Homo sapiens

<400> 16

Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg Met His Pro Asn Val
1 5 10 15

Ser Gln Gly Cys Gln Gly Cys Ala Thr Cys Ser Asp Tyr Asn Gly
20 25 30

Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala Leu Glu Arg Ile Gly
35 40 45

Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys Pro Ser Gly Tyr Tyr
50 55 60

Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr Lys Cys Lys Ala Asp
 65 70 75 80
 Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly
 85 90 95
 Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn Cys Pro Glu Gly Leu
 100 105 110
 Glu Ala Asn Asn His Thr Met Glu Cys Val Ser Ile Val His Cys Glu
 115 120 125
 Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr Lys Lys Gly Lys Thr
 130 135 140
 Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val Arg Glu Ile Ile Gln
 145 150 155 160
 His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro Thr Asn Glu Thr Arg
 165 170 175
 Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys Gly Glu Arg Gly Lys
 180 185 190
 Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn Lys Gly Glu Ser Lys
 195 200 205
 Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser Ser Lys Glu Ile Pro
 210 215 220
 Glu Gln Arg Glu Asn Lys Gln Gln Lys Lys Arg Lys Val Gln Asp
 225 230 235 240
 Lys Gln Lys Ser Val Ser Val Ser Thr Val His
 245 250

<210> 17
 <211> 23

<212> PRT
 <213> Homo sapiens

<400> 17

Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys Lys
 1 5 10 15

Ser Gly Phe Tyr Leu His Leu
 20

<210> 18
 <211> 46

<212> PRT
 <213> Homo sapiens

<400> 18

Ile Asn Lys Cys Thr Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn
1 5 10 15

Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly
20 25 30

Lys Cys Leu Asp Asn Cys Pro Glu Gly Leu Glu Ala Asn Asn
35 40 45

<210> 19
<211> 20

<212> PRT
<213> Homo sapiens

<400> 19

Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys
1 5 10 15

Ser Asp Tyr Asn
20

<210> 20
<211> 37

<212> PRT
<213> Homo sapiens

<400> 20

Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr
1 5 10 15

Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val
20 25 30

Arg Glu Ile Ile Gln
35

<210> 21
<211> 10

<212> PRT
<213> Homo sapiens

<400> 21

Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys
1 5 10

<210> 22
<211> 42

<212> PRT
<213> Homo sapiens

<400> 22

Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys Gly Glu Arg Gly Lys
1 5 10 15

Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn Lys Gly Glu Ser Lys
20 25 30

Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu
35 40

<210> 23

<211> 14

<212> PRT

<213> Homo sapiens

<400> 23

Thr Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly
1 5 10

<210> 24

<211> 20

<212> PRT

<213> Homo sapiens

<400> 24

Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr Lys Lys Gly
1 5 10 15

Lys Thr Cys Gly
20

<210> 25

<211> 229

<212> PRT

<213> Mus musculus

<400> 25

Val Gly Ser Arg Gly Ile Lys Gly Lys Arg Gln Arg Arg Ile Ser Ala
1 5 10 15

Glu Gly Ser Gln Ala Cys Ala Lys Gly Cys Glu Leu Cys Ser Glu Val
20 25 30

Asn Gly Cys Leu Lys Cys Ser Pro Lys Leu Phe Ile Leu Leu Glu Arg
35 40 45

Asn Asp Ile Arg Gln Val Gly Val Cys Leu Pro Ser Cys Pro Pro Gly
50 55 60

Tyr Phe Asp Ala Arg Asn Pro Asp Met Asn Lys Cys Ile Lys Cys Lys
65 70 75 80

Ile Glu His Cys Glu Ala Cys Phe Ser His Asn Phe Cys Thr Lys Cys
85 90 95

Gln Glu Ala Leu Tyr Leu His Lys Gly Arg Cys Tyr Pro Ala Cys Pro
100 105 110

Glu Gly Ser Thr Ala Ala Asn Ser Thr Met Glu Cys Gly Ser Pro Ala
115 120 125

Gln Cys Glu Met Ser Glu Trp Ser Pro Trp Gly Pro Cys Ser Lys Lys
130 135 140

Arg Lys Leu Cys Gly Phe Arg Lys Gly Ser Glu Glu Arg Thr Arg Arg
145 150 155 160

Val Leu His Ala Pro Gly Gly Asp His Thr Thr Cys Ser Asp Thr Lys
165 170 175

Glu Thr Arg Lys Cys Thr Val Arg Arg Thr Pro Cys Pro Glu Gly Gln
180 185 190

Lys Arg Arg Lys Gly Gly Gln Gly Arg Arg Glu Asn Ala Asn Arg His
195 200 205

Pro Ala Arg Lys Asn Ser Lys Glu Pro Arg Ser Asn Ser Arg Arg His
210 215 220

Lys Gly Gln Gln Gln
225

<210> 26
<211> 265

<212> PRT
<213> Homo sapiens

<400> 26

Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met
1 5 10 15

Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg
20 25 30

Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys
35 40 45

Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala
50 55 60

Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys
65 70 75 80

Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr
85 90 95

Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr
100 105 110

Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn
115 120 125

Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser
130 135 140

Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr
145 150 155 160

Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val
165 170 175

Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro
180 185 190

Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys
195 200 205

Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn
210 215 220

Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser
225 230 235 240

Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys
245 250 255

Arg Lys Val Gln Asp Lys Gln Lys Ser
260 265

<210> 27

<211> 8

<212> PRT

<213> Homo sapiens

<400> 27

Ser Val Ser Val Ser Thr Val His
1 5

<210> 28

<211> 7

<212> PRT

<213> Homo sapiens

<400> 28

Val Ser Val Ser Thr Val His
1 5

<210> 29
<211> 27
<212> PRT
<213> Homo sapiens

<400> 29

Gly Ile Glu Val Thr Leu Ala Glu Gly Leu Thr Ser Val Ser Gln Arg
1 5 10 15
Thr Gln Pro Thr Pro Cys Arg Arg Arg Tyr Leu
20 25

<210> 30
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 30

ctcgggaaga agcgcgccat ttgtgttgg 30

<210> 31
<211> 2384
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (511)..(1347)

<220>
<221> misc_feature
<222> (2367)..(2367)
<223> n = A, T, G, or C

<400> 31

ggagcggctc ctgctcagaa cgccagaagc agctcgggtc tctccagcgc cccttgcacca 60
tggctgcgtt acccacggcg tccgcttccc tgcgctcccg ggtccctgc cacagccgca 120
gccgctgcag cctctgagcc ccaggggcca ctgctgcct ggattccgccc cgccagccgccc 180
gctgctgtgc aaccgaggct aacctgcggc cagccaggag gtcctgcac cttcgctcg 240
cgccgatgac agccacccca gagcagccgg ctgtgttcgg acaatttgag aatgcaattg 300
ttgggttccc ggtccaccccg tcccgcttcg cttgccatca cagcacgcct'gttggatctc 360
agtggagaag tcccgcgtct ctgggttttc tactcttcgt atagactcgc ctaacaccta 420
catacatatt tttctttaaa aaaaaacatt aaatataact aacagtggaa agaaaaagga 480

gagaaaaaaag ggaaacatta cagggttact atg cac ttg cga ctg att tct tgt	534		
Met His Leu Arg Leu Ile Ser Cys			
1	5		
ttt ttt atc att ttg aac ttt atg gaa tac att ggc agc caa aac gcc	582		
Phe Phe Ile Ile Leu Asn Phe Met Glu Tyr Ile Gly Ser Gln Asn Ala			
10	15	20	
tcc cga gga agg cgc cag cga aga atg cat cct aat gtc agt caa ggc	630		
Ser Arg Gly Arg Gln Arg Arg Met His Pro Asn Val Ser Gln Gly			
25	30	35	40
tgc caa gga ggc tgt gca acg tgt tca gat tac aat ggc tgt ttg tca	678		
Cys Gln Gly Gly Cys Ala Thr Cys Ser Asp Tyr Asn Gly Cys Leu Ser			
45	50	55	
tgt aag ccc aga ctg ttt gtt ctg gaa agg att ggc atg aag cag	726		
Cys Lys Pro Arg Leu Phe Val Leu Glu Arg Ile Gly Met Lys Gln			
60	65	70	
ata gga gtg tgt ctc tct tcg tgt cca agt gga tat tac gga act cga	774		
Ile Gly Val Cys Leu Ser Ser Cys Pro Ser Gly Tyr Tyr Gly Thr Arg			
75	80	85	
tat cca gat ata aat aaa tgt aca aaa tgc aaa gtt gac tgt gat acc	822		
Tyr Pro Asp Ile Asn Lys Cys Thr Lys Cys Lys Val Asp Cys Asp Thr			
90	95	100	
tgt ttc aac aaa aat ttc tgc aca aag tgt aaa agt gga ttt tac tta	870		
Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly Phe Tyr Leu			
105	110	115	120
cac ctt gga aag tgc ctt gac agt tgc cca gaa ggg tta gaa gcc aac	918		
His Leu Gly Lys Cys Leu Asp Ser Cys Pro Glu Gly Leu Glu Ala Asn			
125	130	135	
aat cat act atg gaa tgt gtc agt att gta cac tgt gag gcc agt gaa	966		
Asn His Thr Met Glu Cys Val Ser Ile Val His Cys Glu Ala Ser Glu			
140	145	150	
tgg agt cca tgg agt cca tgt atg aag aaa gga aaa aca tgt ggc ttc	1014		
Trp Ser Pro Trp Ser Pro Cys Met Lys Lys Gly Lys Thr Cys Gly Phe			
155	160	165	
aaa agg ggg act gaa aca cgg gtc cga gat ata cta cag cat cct tca	1062		
Lys Arg Gly Thr Glu Thr Arg Val Arg Asp Ile Leu Gln His Pro Ser			
170	175	180	
gcc aag ggt aag ggt aac ctg tgc ccc cca acc agc gag aca aga act	1110		
Ala Lys Gly Lys Gly Asn Leu Cys Pro Pro Thr Ser Glu Thr Arg Thr			
185	190	195	200
tgt ata gta caa aga aag aag tgt tca aag gga gag cga gga aaa aag	1158		
Cys Ile Val Gln Arg Lys Lys Cys Ser Lys Gly Glu Arg Gly Lys Lys			
205	210	215	
gga aga gag aga aaa cga aaa aaa ctg aat aaa gaa gaa aga aag gaa	1206		
Gly Arg Glu Arg Lys Arg Lys Lys Leu Asn Lys Glu Glu Arg Lys Glu			
220	225	230	

<210> 32
<211> 279
<212> PRT
<213> *Mus musculus*

Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys
 35 40 45

Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Val
 50 55 60

Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys
 65 70 75 80

Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr
 85 90 95

Lys Cys Lys Val Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr
 100 105 110

Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Ser
 115 120 125

Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser
 130 135 140

Ile Val His Cys Glu Ala Ser Glu Trp Ser Pro Trp Ser Pro Cys Met
 145 150 155 160

Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val
 165 170 175

Arg Asp Ile Leu Gln His Pro Ser Ala Lys Gly Lys Gly Asn Leu Cys
 180 185 190

Pro Pro Thr Ser Glu Thr Arg Thr Cys Ile Val Gln Arg Lys Lys Cys
 195 200 205

Ser Lys Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys
 210 215 220

Leu Asn Lys Glu Glu Arg Lys Glu Thr Ser Ser Ser Ser Asp Ser Lys
 225 230 235 240

Gly Leu Glu Ser Ser Ile Glu Thr Pro Asp Gln Gln Glu Asn Lys Glu
 245 250 255

Arg Gln Gln Gln Gln Lys Arg Arg Ala Arg Asp Lys Gln Gln Lys Ser
 260 265 270

Val Ser Val Ser Thr Val His
 275

<210> 33

<211> 2101

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (259)..(1074)

<400> 33

tcgcggcgat gccagccacc ccagcgaagc cgccgcagtt cagtgcgtgg ataatttgc 60

agtacaatag ttggtttccc tgtccacccg ccccacttcg cttgccatca cagcacgcct 120
 atcgatgtg agaggagaag tcccgctgct cgggactgt ctatatacgc ctaacaccta 180
 catatattt aaaaacatta aatataatta acaatcaaaa gaaagaggag aaaggaaggg 240
 aagcattact gggttact atg cac ttg cga ctg att tct tgg ctt ttt atc 291
 Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile
 1 5 10
 att ttg aac ttt atg gaa tac atc ggc agc caa aac gcc tcc cgg gga 339
 Ile Leu Asn Phe Met Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly
 15 20 25
 agg cgc cag cga aga atg cat cct aac gtt agt caa ggc tgc caa gga 387
 Arg Arg Gln Arg Arg Met His Pro Asn Val Ser Gln Gly Cys Gln Gly
 30 35 40
 ggc tgt gca aca tgc tca gat tac aat gga tgt ttg tca tgt aag ccc 435
 Gly Cys Ala Thr Cys Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro
 45 50 55
 aga cta ttt ttt gct ctg gaa aga att ggc atg aag cag att gga gta 483
 Arg Leu Phe Phe Ala Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val
 60 65 70 75
 tgt ctc tct tca tgt cca agt gga tat tat gga act cga tat cca gat 531
 Cys Leu Ser Ser Cys Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp
 80 85 90
 ata aat aag tgt aca aaa tgc aaa gct gac tgt gat acc tgt ttc aac 579
 Ile Asn Lys Cys Thr Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn
 95 100 105
 aaa aat ttc tgc aca aaa tgt aaa agt gga ttt tac tta cac ctt gga 627
 Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly
 110 115 120
 aag tgc ctt gac aat tgc cca gaa ggg ttg gaa gcc aac aac cat act 675
 Lys Cys Leu Asp Asn Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr
 125 130 135
 atg gag tgt gtc agt att gtg cac tgt gag gtc agt gaa tgg aat cct 723
 Met Glu Cys Val Ser Ile Val His Cys Glu Val Ser Glu Trp Asn Pro
 140 145 150 155
 tgg agt cca tgc acg aag aag gga aaa aca tgt ggc ttc aaa aga ggg 771
 Trp Ser Pro Cys Thr Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly
 160 165 170
 act gaa aca cgg gtc cga gaa ata ata cag cat cct tca gca aag ggt 819
 Thr Glu Thr Arg Val Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly
 175 180 185
 aac cta tgt ccc cca aca aat gag aca aga aag tgt aca gtg caa agg 867
 Asn Leu Cys Pro Pro Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg
 190 195 200
 aag aag tgt cag aag gga gaa cga gga aaa aaa gga agg gag agg aaa 915
 Lys Lys Cys Gln Lys Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys
 205 210 215

aga aaa aaa cct aat aaa gga gaa agt aaa gaa gca ata cct gac agc	963
Arg Lys Lys Pro Asn Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser	
220	225
230	235
aaa agt ctg gaa tcc agc aaa gaa atc cca gag caa cga gaa aac aaa	1011
Lys Ser Leu Glu Ser Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys	
240	245
250	
cag cag cag aag aag cga aaa gtc caa gat aaa cag aaa tcg gta tca	1059
Gln Gln Lys Lys Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser	
255	260
265	
gtc agc act gta cac tagagggttc catgagatta ttgttagactc atgatgctgc	1114
Val Ser Thr Val His	
270	
tatctcaacc agatgcccag gacaggtgct ctagccatta ggaccacaaa tggacatgtc	1174
agttattgct ctgtctaaac aacattccca gtagttgcta tattcttcata acaagcatag	1234
ttaacaacaa agagccaaaa gatcaaagaa gggatacttt cagatggttg tcttgtgtc	1294
ttctctgcat tttaaaaga caagacattc ttgtacatata tatcaatagg ctataagatg	1354
taacaacgaa atgatgacat ctggagaaga aacatcttt ccttataaaaa atgtgtttc	1414
aagctgttgt tttaagaagc aaaagatagt tctgcaaatt caaagataca gtatcccttc	1474
aaaacaaata ggagttcagg gaagagaaac atccttcaaa ggacagtgtt gtttgaccg	1534
ggagatctag agagtgtca gaatttagggc ctggcatttg gaatcacagg atttatcatc	1594
acagaaacaa ctgttttaag attagttcca tcactctcat cctgtatTTT tataagaaac	1654
acaagagtgc ataccagaat tgaatatacc atatggatt ggagaaagac aaatgtggaa	1714
gaaatcatag agctggagac tactttgtg ctttacaaaa ctgtgaagga ttgtggcac	1774
ctggaacagg tctccaatct atgttagcac tatgtggctc agcctctgtt accccttgg	1834
ttatatatca acctgtaaac atgtgcctgt aacttacttc caaaaacaaa atcataactta	1894
ttagaagaaa attctgattt tatagaaaaaa aaatagagca aggagaatat aacatgtttg	1954
caaagtcatg tgtttcttt ctcaatgagg gaaaaacaat tttattacct gcttaatgg	2014
ccacctggaa ctaaaaggga tactatTTT taacaaggta tatcttagtag gggagaaagc	2074
caccacaata aatataattt ttaatag	2101

<210> 34
 <211> 272
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met
 1 5 10 15

Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg
 20 25 30

Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys
 35 40 45

Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala
 50 55 60

Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys
 65 70 75 80

Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr
 85 90 95

Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr
 100 105 110

Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn
 115 120 125

Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser
 130 135 140

Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr
 145 150 155 160

Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val
 165 170 175

Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro
 180 185 190

Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys
 195 200 205

Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn
 210 215 220

Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser
 225 230 235 240

Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Lys Lys
 245 250 255

Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val His
 260 265 270

<210> 35
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 35
 agtacaaaga aagaagtgtt c

<210> 36
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 36
ttagtctaca gtaacctcgc a 21

<210> 37
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 37
taatacgaact cactataggg 20

<210> 38
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 38
tcgcggcgat gccagccacc ccag 24

<210> 39
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 39
agcacgccta tcggatgtga gaggagaagt 30

<210> 40
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 40
ctattaacaa atatatttat tgtggtggct 30

<210> 41

<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 41
tggtggcttt ctccccctact agatatacct 30

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 42
gatttttaggt gacactatacg 20

<210> 43
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 43
ccgctcgagc caccatgcac ttgcgactga tttc 34

<210> 44
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 44
attgaattcc tagtgtacag tgctgactg 29

<210> 45
<211> 84
<212> DNA
<213> Homo sapiens

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<221> CDS
<222> (1)..(81)

<400> 45

ggg att gaa gtc acc cta gct gaa ggc ctc acc agt gtt tca cag agg 48
Gly Ile Glu Val Thr Leu Ala Glu Gly Leu Thr Ser Val Ser Gln Arg
1 5 10 15

aca cag ccc acc cct tgc agg agg agg tat ctc tga 84
Thr Gln Pro Thr Pro Cys Arg Arg Arg Tyr Leu
20 25

<210> 46
<211> 27
<212> PRT
<213> Homo sapiens

<400> 46
Gly Ile Glu Val Thr Leu Ala Glu Gly Leu Thr Ser Val Ser Gln Arg
1 5 10 15
Thr Gln Pro Thr Pro Cys Arg Arg Arg Tyr Leu
20 25

<210> 47
<211> 1436
<212> DNA
<213> Homo sapiens

<400> 47
cccgccggct cctggAACCC cggttcgCGG cGATGCCAGC cACCCAGCG aAGCCGCCGC 60
aGTCAGTGC ttggataatt tGAAAGTACA aTAGTTGGTT tCCCTGTCCA cCCGCCCCAC 120
ttcgcTTGCC atcacAGCAC gcctatCGGA tGTGAGAGGA gaAGTCCCGC tgctcgggca 180
ctgtctatac acgcctaaca cctacatata tttaaaaAC attaaatata attaacaATC 240
aaaAGAAAGA ggagaaAGGA aggGAAGCAT tactGGGTTA ctatGCACTT gCGACTGATT 300
tcttggctt ttatcatttt gaactttatG gaatacatG gcAGCCAAA CGCCTCCGG 360
ggaaggcgcc agcgaagaat gcatcctaAC gttAGTCAAG gctGCCAAGG aggCTGTGCA 420
acatGCTCAG attacaatGG atgtttgtca tGtaAGCCCA gactatttt tgctctggaa 480
agaattggca tgaAGCAGAT tggAGTATGT ctctcttcat gtcCAAGTGG atattatggA 540
actcgatATC cAGATAAAA taAGTGTACA aaATGCAAAG ctGACTGTGA tacctgttC 600
aacaAAAAtt tctgcacAAA atgtAAAAGT ggattttACT tacacCTTGG aaAGTGCCTT 660
gacaattGCC cagaAGGGTT ggaAGCCAAc aaccatacta tggAGTGTGT cAGTATTGTG 720
cactgtgagg tcAGTGAATG gaatCCTTGG agtCCATGCA cgaAGAAGGG aAAAACATGT 780
ggcttcaAAA gagggACTGA aacacGGGTC cgAGAAATAA tacAGCATCC ttcAGCAAAG 840
ggtaacctgt gtcccccaAC aaATGAGACA agAAAGTGTa cAGTGCaaAG gaAGAAGTGT 900
cagaAGGGAG aacgAGGAAA AAAAGGAAGG gagAGGAAA gaaaaAAACC taataAGGA 960

gaaagtaaag aagcaatacc tgacagcaaa agtctggaat ccagcaaaga aatcccagag 1020
caacgagaaa acaaacagca gcagaagaag cgaaaagtcc aagataaaca gaaatcgggg 1080
attgaagtca ccctagctga aggcctcacc agtgttcac agaggacaca gcccacccct 1140
tgcaggagga ggtatctctg agtgcgc acagaatcgc atgacccacc ttaaccttcc 1200
tgttgtcatg gaaggatgca cggctgctct gtccactgtg attcctagcc ctctcaagat 1260
cactgctttc tgaagaattt gcaatgactc tggcttctgg ctgcttatct ctggacaccc 1320
gttctccacc agttgtacag ttcatgtaat ctacttgct taattgattt tccacttctc 1380
tcttcctctt ctaagatata aacattttaa atgatttaaa aaaaaaaaaa aaaaaa 1436

<210> 48
<211> 292
<212> PRT
<213> Homo sapiens

<400> 48
Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met
1 5 10 15
Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg
20 25 30
Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Cys Ala Thr Cys
35 40 45
Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala
50 55 60
Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys
65 70 75 80
Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr
85 90 95
Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr
100 105 110
Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn
115 120 125
Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser
130 135 140
Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr
145 150 155 160
Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val
165 170 175
Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro
180 185 190
Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys
195 200 205

Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Pro Asn
210 215 220

Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser
225 230 235 240

Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys
245 250 255

Arg Lys Val Gln Asp Lys Gln Lys Ser Gly Ile Glu Val Thr Leu Ala
260 265 270

a Glu Gly Leu Thr Ser Val Ser Gln Arg Thr Gln Pro Thr Pro Cys Arg
275 280 285

cont Arg Arg Tyr Leu
290